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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/092,880

DATE: 03/26/2002
TIME: 13:16:51

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\03262002\J092880.raw

3 <110> APPLICANT: Barenkamp, Stephen J.
5 <120> TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
6 HAEMOPHILUS
W--> 8 <130> FILE REFERENCE:
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/092,880
C--> 11 <141> CURRENT FILING DATE: 2002-03-08
13 <150> PRIOR APPLICATION NUMBER: 09/155,614
14 <151> PRIOR FILING DATE: 1998-09-30
16 <150> PRIOR APPLICATION NUMBER: 08/617,697
17 <151> PRIOR FILING DATE: 1996-04-01
19 <150> PRIOR APPLICATION NUMBER: PCT/US97/04707
20 <151> PRIOR FILING DATE: 1997-04-01
22 <160> NUMBER OF SEQ ID NOS: 11
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 5116
28 <212> TYPE: DNA
29 <213> ORGANISM: Haemophilus influenzae
31 <400> SEQUENCE: 1
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33 cacctttttt gcagtcata tgcaaatatt ttaaaaaata gtataaatcc gccatataaaa 120
34 atggtataat ctttcatctt tcataatca tcttcatct ttcataatcc atcttcatc 180
35 tttcatctt catcttcat ctttcatctt tcataatca tcttcatct ttcataatcc 240
36 acatgccctg atgaaccgag ggaagggagg gaggggcaag aatgaagagg gagctgaacg 300
37 aacgcaatg ataaagtaat ttaattgttc aactaacctt aggagaaaaat atgaacaacg 360
38 tatatcgct caaattcagc aaacgcctga atgcttttgt tgctgtgtc gaattggcac 420
39 ggggttgtga ccattccaca gaaaaaggca gcgaaaaacc tgctcgatg aaagtgcgtc 480
40 acttagcggt aaagccactt tccgctatgt tactatctt aggtgtacaa tctattccac 540
41 aatctgtttt agcaagcgcc ttacaaggaa tggatgttagt acacggcaca gcccactatgc 600
42 aagtagatgg taataaaacc attatccgca acagtgttgc cgatatcatt aattggaaac 660
43 aatttaacat cgaccaaaat gaaatggtgc agttttaca agaaaaacaac aactccgccc 720
44 tattcaaccc tgttacatct aaccaaattt cccaaataaa agggatttttta gattctaacg 780
45 gacaagtctt ttaatcaac ccaaatttgc tcacaatagg taaagacgcgca attattaaca 840
46 ctaatggctt tacggcttct acgcttagaca tttctaaacgc aaacatcaag gcgctgtt 900
47 tcacccctgcg gcaaaacccaa gataaaggcgc tcgctgaaat tgtgaatcac ggtttaaattt 960
48 ctgtcggtaa agacggcagt gtaaaatctt ttggtggcaa agtggaaaaac gagggtgtga 1020
49 ttagcgtaaa tggtggcagc atttctttac tcgcaggggca aaaaatcacc atcagcgata 1080
50 taataaaaccc aaccattact tacagcattt cccgcctgaa aatgaagcg gtcaatctgg 1140
51 gcgatatttt tgccaaaggc ggttaacattt atgtccgtgc tgccactatt cgaaaccaag 1200
52 gtaaaacttgc tgctgattct gtaagcaaaag ataaaaggcg caatattgtt cttccgcaca 1260
53 aagagggtgtgaaatggcggaaatt ggcgggtgtaa tttccgctca aaatcagcata gctaaaggcg 1320
54 gcaagctgat gattacagggc gataaagtca cattaaaaac aggtgcagtt atcgaccttt 1380
55 caggtaaaga agggggagaa acttaccttgc gcggtgacgc gcgccggcga ggtaaaaaq 1440

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56 gcattcaatt agcaaagaaa acctcttag aaaaaggctc aaccatcaat gtatcaggca 1500
 57 aagaaaaagg cgacgcgcattgtgtggg gcgatattgc gttatttgac ggcaatatta 1560
 58 acgctcaagg tagtggtgat atcgctaaaa ccgggtggttt tggagacg tcggggcatg 1620
 59 atttattcat caaagacaat gcaattgtt acgccaaaga gtggttgtt aaccggata 1680
 60 atgtatctat taatgcagaa acagcaggac gcagcaatac ttcagaagac gatgaataca 1740
 61 cgggatccgg gaatagtgcg agcacccaa aacgaaacaa agaaaagaca acattaacaa 1800
 62 acacaactct tgagagtata ctaaaaaaag gtaccttgc taacatcaact gctaatac 1860
 63 gcatctatgt caatagctcc attaatttat ccaatggcag cttactt tggagtgg 1920
 64 gtccggagcg 1980
 65 gtccaaactt aacaatttac tcaggcggct gggttgcgt tcataaaaat atctcaactcg 2040
 66 gggcgcaagg taacataaac attacagcta aacaagat 2100
 67 accaagtcat tacaggtcaa gggacttta cctcaggcaa tcaaaaaggt ttttagattt 2160
 68 ataatgtctc tctaaacgcg 2220
 69 aatacgctat cacaataaa tttgaaggga cttaaatat ttcaggggaa gtgaacatct 2280
 70 caatggttt acctaaaaat gaaagtggat atgataaaatt caaaggacgc acttactgga 2340
 71 atttaacctc cttaatgtt tccgagatgc gcgagttt cctcactatt gactccagag 2400
 72 gaagcgatag tgcaggcaca 2460
 73 aagacactac cttaatgtt gaacgaaatg 2520
 74 tagggataaa taagtatttgc agtttgcattt accatcattt taatggaaac atttcagttt 2580
 75 cgggggggg 2640
 76 gtgtatgtt 2700
 77 cttaggcgc 2760
 78 gaggcaacat 2820
 79 tagccaaaaaa 2880
 80 taacagaaat 2940
 81 cggatgtt 2960
 82 gcaaccccttac 3000
 83 acgtaattt 3060
 84 aaggcaattt 3120
 85 ccaagaattt 3180
 86 atataacca 3240
 87 aaattggcgg 3300
 88 atattacca 3360
 89 cgacaaacaa 3420
 90 atatttcagg 3480
 91 gtaacaccaa 3540
 92 attcaaaaaat 3600
 93 gtagtaataa 3660
 94 aaaatgtaac 3720
 95 gtggagaaat 3780
 96 taaccgc 3840
 97 ttactgcaac 3900
 98 ctgcaaatag 3960
 99 taaccacttc 4020
 100 ttaaagcaac 4080
 101 aggctaactgt 4140
 102 atgttacggc 4200
 103 aaggagctgc 4260
 104 ttacttcagc 4320
 105 caagggtcag 4380

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105 ttaatgccgc caatgtgaca ctaaatacta caggcactt aactaccgtg aagggttcaa 4440
106 acattaaatgc aaccagcggt accttggta ttaacgc当地 agacgctgag ctaaatggcg 4500
107 cagcattggg taaccacaca gtggtaatg caaccaacgc aaatggctcc ggcagcgtaa 4560
108 tcgcgacaac ctcagcaga gtgaacatca ctggggattt aatcacaata aatggattaa 4620
109 atatcatttc aaaaaacggt ataaacaccg tactgttaaa aggcgttaaa attgatgtga 4680
110 aatacattca accgggtata gcaagcgtag atgaagtaat tgaagc当地 cgcatccttg 4740
111 agaaggtaaa agatttatct gatgaagaaa gagaagcgtt agctaaactt ggagtaagtg 4800
112 ctgtacgtt tattgagcca aataatacaa ttacagtcga tacacaaaat gaatttgcaa 4860
113 ccagaccatt aagtgc当地 gtgatttctg aaggcaggc当地 gtgatttctca aacagtgatg 4920
114 ggc当地 acgggt gtgc当地 taat atcgc当地 acggc当地 ggtaaagg 4980
115 tagatttcat cctgcaatga agtc当地 ttaattcgtatt atttactgtg tgggttaaag 5040
116 ttcatgtacgg gcttaccacca tctttaaaa aattacggag aataacaataa agtattttta 5100
117 acagggttattt attatg 5116
120 <210> SEQ ID NO: 2
121 <211> LENGTH: 1536
122 <212> TYPE: PRT
123 <213> ORGANISM: Haemophilus influenzae
125 <400> SEQUENCE: 2
126 Met Asn Lys Ile Tyr Arg Leu Lys Phe Ser Lys Arg Leu Asn Ala Leu
127 1 5 10 15
129 Val Ala Val Ser Glu Leu Ala Arg Gly Cys Asp His Ser Thr Glu Lys
130 20 25 30
132 Gly Ser Glu Lys Pro Ala Arg Met Lys Val Arg His Leu Ala Leu Lys
133 35 40 45
135 Pro Leu Ser Ala Met Leu Leu Ser Leu Gly Val Thr Ser Ile Pro Gln
136 50 55 60
138 Ser Val Leu Ala Ser Gly Leu Gln Gly Met Asp Val Val His Gly Thr
139 65 70 75 80
141 Ala Thr Met Gln Val Asp Gly Asn Lys Thr Ile Ile Arg Asn Ser Val
142 85 90 95
144 Asp Ala Ile Ile Asn Trp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met
145 100 105 110
147 Val Gln Phe Leu Gln Glu Asn Asn Ser Ala Val Phe Asn Arg Val
148 115 120 125
150 Thr Ser Asn Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly
151 130 135 140
153 Gln Val Phe Leu Ile Asn Pro Asn Gly Ile Thr Ile Gly Lys Asp Ala
154 145 150 155 160
156 Ile Ile Asn Thr Asn Gly Phe Thr Ala Ser Thr Leu Asp Ile Ser Asn
157 165 170 175
159 Glu Asn Ile Lys Ala Arg Asn Phe Thr Phe Glu Gln Thr Lys Asp Lys
160 180 185 190
162 Ala Leu Ala Glu Ile Val Asn His Gly Leu Ile Thr Val Gly Lys Asp
163 195 200 205
165 Gly Ser Val Asn Leu Ile Gly Gly Lys Val Lys Asn Glu Gly Val Ile
166 210 215 220
168 Ser Val Asn Gly Gly Ser Ile Ser Leu Leu Ala Gly Gln Lys Ile Thr
169 225 230 235 240
171 Ile Ser Asp Ile Ile Asn Pro Thr Ile Thr Tyr Ser Ile Ala Ala Pro

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172	245	250	255
174	Glu Asn Glu Ala Val Asn Leu Gly Asp Ile Phe Ala Lys Gly Gly Asn		
175	260	265	270
177	Ile Asn Val Arg Ala Ala Thr Ile Arg Asn Gln Gly Lys Leu Ser Ala		
178	275	280	285
180	Asp Ser Val Ser Lys Asp Lys Ser Gly Asn Ile Val Leu Ser Ala Lys		
181	290	295	300
183	Glu Gly Glu Ala Glu Ile Gly Gly Val Ile Ser Ala Gln Asn Gln Gln		
184	305	310	315
186	Ala Lys Gly Gly Lys Leu Met Ile Thr Gly Asp Lys Val Thr Leu Lys		
187	325	330	335
189	Thr Gly Ala Val Ile Asp Leu Ser Gly Lys Glu Gly Gly Glu Thr Tyr		
190	340	345	350
192	Leu Gly Gly Asp Glu Arg Gly Glu Gly Lys Asn Gly Ile Gln Leu Ala		
193	355	360	365
195	Lys Lys Thr Ser Leu Glu Lys Gly Ser Thr Ile Asn Val Ser Gly Lys		
196	370	375	380
198	Glu Lys Gly Gly Arg Ala Ile Val Trp Gly Asp Ile Ala Leu Ile Asp		
199	385	390	395
201	400	405	410
202	Gly Asn Ile Asn Ala Gln Gly Ser Gly Asp Ile Ala Lys Thr Gly Gly		
204	420	425	430
207	Phe Val Glu Thr Ser Gly His Asp Leu Phe Ile Lys Asp Asn Ala Ile		
208	435	440	445
210	Val Asp Ala Lys Glu Trp Leu Leu Asp Phe Asp Asn Val Ser Ile Asn		
211	450	455	460
213	Ala Glu Thr Ala Gly Arg Ser Asn Thr Ser Glu Asp Asp Glu Tyr Thr		
214	465	470	475
216	Gly Ser Gly Asn Ser Ala Ser Thr Pro Lys Arg Asn Lys Glu Lys Thr		
217	485	490	495
219	Thr Leu Thr Asn Thr Thr Leu Glu Ser Ile Leu Lys Lys Gly Thr Phe		
220	500	505	510
222	Val Asn Ile Thr Ala Asn Gln Arg Ile Tyr Val Asn Ser Ser Ile Asn		
223	515	520	525
225	Leu Ser Asn Gly Ser Leu Thr Leu Trp Ser Glu Gly Arg Ser Gly Gly		
226	530	535	540
228	Gly Val Glu Ile Asn Asn Asp Ile Thr Thr Gly Asp Asp Thr Arg Gly		
229	545	550	555
231	Ala Asn Leu Thr Ile Tyr Ser Gly Gly Trp Val Asp Val His Lys Asn		
232	565	570	575
234	Ile Ser Leu Gly Ala Gln Gly Asn Ile Asn Ile Thr Ala Lys Gln Asp		
235	580	585	590
237	Ile Ala Phe Glu Lys Gly Ser Asn Gln Val Ile Thr Gly Gln Gly Thr		
238	595	600	605
240	238 Ile Thr Ser Gly Asn Gln Lys Gly Phe Arg Phe Asn Asn Val Ser Leu		
241	610	615	620
243	Asn Gly Thr Gly Ser Gly Leu Gln Phe Thr Thr Lys Arg Thr Asn Lys		
244	625	630	635
			640

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246 Val Asn Ile Ser Met Val Leu Pro Lys Asn Glu Ser Gly Tyr Asp Lys
247 645 650 655
249 Phe Lys Gly Arg Thr Tyr Trp Asn Leu Thr Ser Leu Asn Val Ser Glu
250 660 665 670
252 Ser Gly Glu Phe Asn Leu Thr Ile Asp Ser Arg Gly Ser Asp Ser Ala
253 675 680 685
255 Gly Thr Leu Thr Gln Pro Tyr Asn Leu Asn Gly Ile Ser Phe Asn Lys
256 690 695 700
258 Asp Thr Thr Phe Asn Val Glu Arg Asn Ala Arg Val Asn Phe Asp Ile
259 705 710 715 720
261 Lys Ala Pro Ile Gly Ile Asn Lys Tyr Ser Ser Leu Asn Tyr Ala Ser
262 725 730 735
264 Phe Asn Gly Asn Ile Ser Val Ser Gly Gly Ser Val Asp Phe Thr
265 740 745 750
267 Leu Leu Ala Ser Ser Ser Asn Val Gln Thr Pro Gly Val Val Ile Asn
268 755 760 765
270 Ser Lys Tyr Phe Asn Val Ser Thr Gly Ser Ser Leu Arg Phe Lys Thr
271 770 775 780
273 Ser Gly Ser Thr Lys Thr Gly Phe Ser Ile Glu Lys Asp Leu Thr Leu
274 785 790 795 800
276 Asn Ala Thr Gly Gly Asn Ile Thr Leu Leu Gln Val Glu Gly Thr Asp
277 805 810 815
279 Gly Met Ile Gly Lys Gly Ile Val Ala Lys Lys Asn Ile Thr Phe Glu
280 820 825 830
282 Gly Gly Asn Ile Thr Phe Gly Ser Arg Lys Ala Val Thr Glu Ile Glu
283 835 840 845
285 Gly Asn Val Thr Ile Asn Asn Ala Asn Val Thr Leu Ile Gly Ser
286 850 855 860
288 Asp Phe Asp Asn His Gln Lys Pro Leu Thr Ile Lys Lys Asp Val Ile
289 865 870 875 880
291 Ile Asn Ser Gly Asn Leu Thr Ala Gly Asn Ile Val Asn Ile Ala
292 885 890 895
294 Gly Asn Leu Thr Val Glu Ser Asn Ala Asn Phe Lys Ala Ile Thr Asn
295 900 905 910
297 Phe Thr Phe Asn Val Gly Leu Phe Asp Asn Lys Gly Asn Ser Asn
298 915 920 925
300 Ile Ser Ile Ala Lys Gly Gly Ala Arg Phe Lys Asp Ile Asp Asn Ser
301 930 935 940
303 Lys Asn Leu Ser Ile Thr Thr Asn Ser Ser Thr Tyr Arg Thr Ile
304 945 950 955 960
306 Ile Ser Gly Asn Ile Thr Asn Lys Asn Gly Asp Leu Asn Ile Thr Asn
307 965 970 975
309 Glu Gly Ser Asp Thr Glu Met Gln Ile Gly Gly Asp Val Ser Gln Lys
310 980 985 990
312 Glu Gly Asn Leu Thr Ile Ser Ser Asp Lys Ile Asn Ile Thr Lys Gln
313 995 1000 1005
315 Ile Thr Ile Lys Ala Gly Val Asp Gly Glu Asn Ser Asp Ser Asp Ala
316 1010 1015 1020
318 Thr Asn Asn Ala Asn Leu Thr Ile Lys Thr Lys Glu Leu Lys Leu Thr

VERIFICATION SUMMARY
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L:8 M:201 W: Mandatory field data missing, FILE REFERENCE
L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date